SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Reed, John

    (ii) TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

    (iii) NUMBER OF SEQUENCES: 29

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: LONG, ALDRIDGE & NORMAN LLP

        (B) STREET: Suite 600, 701 Pennsylvania Avenue, N.W.
        (C) CITY: Washington
        (D) STATE: District of Columbia
        (E) COUNTRY: U.S.A.
        (F) ZIP: 20004

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/465,485
        (B) FILING DATE: 05-JUN-1995
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/124,256
        (B) FILING DATE: 20-SEP-1993

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 07/840,716
        (B) FILING DATE: 21-FEB-1992

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 07/288,692
        (B) FILING DATE: 22-DEC-1988

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Steven B. Kelber
        (B) REGISTRATION NUMBER: 30,073
        (C) REFERENCE/DOCKET NUMBER: 3335-075-55 CONT

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (202) 624-1200
        (B) TELEFAX: (202) 624-1298

SEQUENCE LISTING

(1) GENERAL INFORMATION:

  (i) APPLICANT: Reed, John

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  (vii) PRIOR APPLICATION DATA:
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     (B) FILING DATE: 22-DEC-1988

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     (A) NAME: Steven B. Kelber
     (B) REGISTRATION NUMBER: 30,073
     (C) REFERENCE/DOCKET NUMBER: 3335-075-55 CONT

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: (202) 624-1200
     (B) TELEFAX: (202) 624-1298

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTCCC   20

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTTCCTCT GGGAAGGATG GCGCACGCTG GGAGA   35

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATGCACCTA CCCAGCCTCC   20

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACGGGGTACG GAGGCTGGGT AGGTGCATCT GGT   33

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAAGGCAT CCTGCAGTTG   20

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCCCAACTG CAGGATGCCT TTGTGGAACT GTACGG   36

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAAGGATG GCGCACGCTG   20

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCGTGCGAC CCTCTTG   17

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACCGCGTGC GACCCTC   17

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iv) ANTI-SENSE: YES

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCCTACCGCG TGCGACC 17

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iv) ANTI-SENSE: YES

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTTCCTACC GCGTGCG 17

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iv) ANTI-SENSE: YES

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCCTTCCT ACCGCGT 17

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACCCTT CCTACCG   17

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGCGGCAG CGCGG   15

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iv) ANTI-SENSE: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGCGGGGCG ACGGA   15

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iv) ANTI-SENSE: YES

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGGAGCGCG GCGGGC   16

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCTCCCAGCG TGCGCCAT   18

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCACTCACG CTCGGCCT   18

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5086 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
GCGCCCGCCC CTCCGCGCCG CCTGCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC      60

GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC     120

TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA     180

CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG     240

GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGAGAACTT CGTAGCAGTC      300

ATCCTTTTTA GGAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC      360

CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG     420

TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC     480

AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT     540

CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT     600

GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT     660

GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT     720

CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG     780

AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA     840

TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG     900

GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC     960

TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA    1020

AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC    1080

TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA    1140

CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA    1200

CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA    1260

AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA    1320

GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT    1380

CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCGTT     1440

GCTTTTCCTC TGGGAAGGAT GGCGCACGCT GGGAGAACGG GGTACGACAA CCGGGAGATA    1500

GTGATGAAGT ACATCCATTA TAAGCTGTCG CAGAGGGGCT ACGAGTGGGA TGCGGGAGAT    1560

GTGGGCGCCG CGCCCCCGGG GGCCGCCCCC GCACCGGGCA TCTTCTCCTC CCAGCCCGGG    1620

CACACGCCCC ATCCAGCCGC ATCCCGCGAC CCGGTCGCCA GGACCTCGCC GCTGCAGACC    1680
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-9-

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CCGGCTGCCC CCGGCGCCGC CGCGGGGCCT GCGCTCAGCC CGGTGCCACC TGTGGTCCAC    1740

CTGGCCCTCC GCCAAGCCGG CGACGACTTC TCCCGCCGCT ACCGCGGCGA CTTCGCCGAG    1800

ATGTCCAGCC AGCTGCACCT GACGCCCTTC ACCGCGCGGG GACGCTTTGC CACGGTGGTG    1860

GAGGAGCTCT TCAGGGACGG GGTGAACTGG GGGAGGATTG TGGCCTTCTT TGAGTTCGGT    1920

GGGGTCATGT GTGTGGAGAG CGTCAACCGG GAGATGTCGC CCTGGTGGA CAACATCGCC     1980

CTGTGGATGA CTGAGTACCT GAACCGGCAC CTGCACACCT GGATCCAGGA TAACGGAGGC    2040

TGGGATGCCT TTGTGGAACT GTACGGCCCC AGCATGCGGC CTCTGTTTGA TTTCTCCTGG    2100

CTGTCTCTGA AGACTCTGCT CAGTTTGGCC CTGGTGGGAG CTTGCATCAC CCTGGGTGCC    2160

TATCTGAGCC ACAAGTGAAG TCAACATGCC TGCCCCAAAC AAATATGCAA AAGGTTCACT    2220

AAAGCAGTAG AAATAATATG CATTGTCAGT GATGTACCAT GAAACAAAGC TGCAGGCTGT    2280

TTAAGAAAAA ATAACACACA TATAAACATC ACACACACAG ACAGACACAC ACACACAA     2340

CAATTAACAG TCTTCAGGCA AAACGTCGAA TCAGCTATTT ACTGCCAAAG GGAAATATCA    2400

TTTATTTTTT ACATTATTAA GAAAAAGAT TTATTTATTT AAGACAGTCC CATCAAAACT     2460

CCGTCTTTGG AAATCCGACC ACTAATTGCC AAACACCGCT TCGTGTGGCT CCACCTGGAT    2520

GTTCTGTGCC TGTAAACATA GATTCGCTTT CCATGTTGTT GGCCGGATCA CCATCTGAAG    2580

AGCAGACGGA TGGAAAAGG ACCTGATCAT TGGGGAAGCT GGCTTTCTGG CTGCTGGAGG     2640

CTGGGGAGAA GGTGTTCATT CACTTGCATT TCTTTGCCCT GGGGGCGTGA TATTAACAGA    2700

GGGAGGGTTC CCGTGGGGGG AAGTCCATGC CTCCCTGGCC TGAAGAAGAG ACTCTTTGCA    2760

TATGACTCAC ATGATGCATA CCTGGTGGGA GGAAAGAGT TGGGAACTTC AGATGGACCT     2820

AGTACCCACT GAGATTTCCA CGCCGAAGGA CAGCGATGGG AAAAATGCCC TTAAATCATA    2880

GGAAAGTATT TTTTTAAGCT ACCAATTGTG CCGAGAAAG CATTTTAGCA ATTTATACAA     2940

TATCATCCAG TACCTTAAAC CCTGATTGTG TATATTCATA TATTTTGGAT ACGCACCCCC    3000

CAACTCCCAA TACTGGCTCT GTCTGAGTAA GAAACAGAAT CCTCTGGAAC TTGAGGAAGT    3060

GAACATTTCG GTGACTTCCG ATCAGGAAGG CTAGAGTTAC CCAGAGCATC AGGCCGCCAC    3120

AAGTGCCTGC TTTTAGGAGA CCGAAGTCCG CAGAACCTAC CTGTGTCCCA GCTTGGAGGC    3180

CTGGTCCTGG AACTGAGCCG GGCCCTCACT GGCCTCCTCC AGGGATGATC AACAGGGTAG    3240

TGTGGTCTCC GAATGTCTGG AAGCTGATGG ATGGAGCTCA GAATTCCACT GTCAAGAAAG    3300

AGCAGTAGAG GGGTGTGGCT GGGCCTGTCA CCCTGGGGCC CTCCAGGTAG GCCCGTTTTC    3360

ACGTGGAGCA TAGGAGCCAC GACCCTTCTT AAGACATGTA TCACTGTAGA GGGAAGGAAC    3420
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AGAGGCCCTG GGCCTTCCTA TCAGAAGGAC ATGGTGAAGG CTGGGAACGT GAGGAGAGGC    3480

AATGGCCACG GCCCATTTTG GCTGTAGCAC ATGGCACGTT GGCTGTGTGG CCTTGGCCAC    3540

CTGTGAGTTT AAAGCAAGGC TTTAAATGAC TTTGGAGAGG GTCACAAATC CTAAAAGAAG    3600

CATTGAAGTG AGGTGTCATG GATTAATTGA CCCCTGTCTA TGGAATTACA TGTAAACAT     3660

TATCTTGTCA CTGTAGTTTG GTTTTATTTG AAAACCTGAC AAAAAAAAAG TTCCAGGTGT    3720

GGAATATGGG GGTTATCTGT ACATCCTGGG GCATTAAAAA AAAATCAATG GTGGGGAACT    3780

ATAAAGAAGT AACAAAAGAA GTGACATCTT CAGCAAATAA ACTAGGAAAT TTTTTTTTCT    3840

TCCAGTTTAG AATCAGCCTT GAAACATTGA TGGAATAACT CTGTGGCATT ATTGCATTAT    3900

ATACCATTTA TCTGTATTAA CTTTGGAATG TACTCTGTTC AATGTTTAAT GCTGTGGTTG    3960

ATATTTCGAA AGCTGCTTTA AAAAAATACA TGCATCTCAG CGTTTTTTTG TTTTTAATTG    4020

TATTTAGTTA TGGCCTATAC ACTATTTGTG AGCAAGGTG ATCGTTTTCT GTTTGAGATT      4080

TTTATCTCTT GATTCTTCAA AAGCATTCTG AGAAGGTGAG ATAAGCCCTG AGTCTCAGCT    4140

ACCTAAGAAA AACCTGGATG TCACTGGCCA CTGAGGAGCT TTGTTTCAAC CAAGTCATGT    4200

GCATTTCCAC GTCAACAGAA TTGTTTATTG TGACAGTTAT ATCTGTTGTC CCTTTGACCT    4260

TGTTTCTTGA AGGTTTCCTC GTCCCTGGGC AATTCCGCAT TTAATTCATG GTATTCAGGA    4320

TTACATGCAT GTTTGGTTAA ACCCATGAGA TTCATTCAGT TAAAAATCCA GATGGCGAAT    4380

GACCAGCAGA TTCAAATCTA TGGTGGTTTG ACCTTTAGAG AGTTGCTTTA CGTGGCCTGT    4440

TTCAACACAG ACCCACCCAG AGCCCTCCTG CCCTCCTTCC GCGGGGGCTT TCTCATGGCT    4500

GTCCTTCAGG GTCTTCCTGA AATGCAGTGG TCGTTACGCT CCACCAAGAA AGCAGGAAAC    4560

CTGTGGTATG AAGCCAGACC TCCCCGGCGG GCCTCAGGGA ACAGAATGAT CAGACCTTTG    4620

AATGATTCTA ATTTTTAAGC AAAATATTAT TTTATGAAAG GTTTACATTG TCAAAGTGAT    4680

GAATATGGAA TATCCAATCC TGTGCTGCTA TCCTGCCAAA ATCATTTTAA TGGAGTCAGT    4740

TTGCAGTATG CTCCACGTGG TAAGATCCTC CAAGCTGCTT TAGAAGTAAC AATGAAGAAC    4800

GTGGACGTTT TTAATATAAA GCCTGTTTTG TCTTTTGTTG TTGTTCAAAC GGGATTCACA    4860

GAGTATTTGA AAAATGTATA TATATTAAGA GGTCACGGGG CTAATTGCT AGCTGGCTGC      4920

CTTTTGCTGT GGGGTTTTGT TACCTGGTTT TAATAACAGT AAATGTGCCC AGCCTCTTGG    4980

CCCCAGAACT GTACAGTATT GTGGCTGCAC TTGCTCTAAG AGTAGTTGAT GTTGCATTTT    5040

CCTTATTGTT AAAAACATGT TAGAAGCAAT GAATGTATAT AAAAGC                    5086
```

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(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 717 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..717

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC CGG GAG ATA GTG ATG      48
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1               5                  10                  15

AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC TAC GAG TGG GAT GCG      96
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
                20                  25                  30

GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC CCC GCA CCG GGC ATC     144
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
            35                  40                  45

TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA GCC GCA TCC CGC GAC     192
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
        50                  55                  60

CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG GCT GCC CCC GGC GCC     240
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65                  70                  75                  80

GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT GTG GTC CAC CTG GCC     288
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85                  90                  95

CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC TAC CGC GGC GAC TTC     336
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
                100                 105                 110

GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC TTC ACC GCG CGG GGA     384
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
            115                 120                 125

CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG GAC GGG GTG AAC TGG     432
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
        130                 135                 140

GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG GTC ATG TGT GTG GAG     480
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160
```

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```
AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC AAC ATC GCC CTG TGG      528
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
                165                 170                 175

ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC TGG ATC CAG GAT AAC      576
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
                180                 185                 190

GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC CCC AGC ATG CGG CCT      624
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
                195                 200                 205

CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT CTG CTC AGT TTG GCC      672
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
        210                 215                 220

CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT CTG AGC CAC AAG          717
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys        .
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:21:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 239 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: protein

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
  1               5               10              15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
            20              25              30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
        35              40              45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
    50              55              60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65              70              75              80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
            85              90              95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
            100             105             110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
        115             120             125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
        130             135             140
```
-13-

```
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145             150             155             160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
            165             170             175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
            180             185             190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
        195             200             205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
    210             215             220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
225             230             235
```

(2)   INFORMATION FOR SEQ ID NO:22:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 615 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: DNA (genomic)

    (ix)   FEATURE:
        (A)   NAME/KEY: CDS
        (B)   LOCATION: 1..615

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC CGG GAG ATA GTG ATG      48
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1               5               10              15

AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC TAC GAG TGG GAT GCG      96
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
            20              25              30

GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC CCC GCA CCG GGC ATC     144
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
            35              40              45

TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA GCC GCA TCC CGC GAC     192
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
    50              55              60

CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG GCT GCC CCC GGC GCC     240
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65              70              75              80
```

```
GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT GTG GTC CAC CTG GCC        288
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85                  90                  95

CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC TAC CGC GGC GAC TTC        336
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
               100                 105                 110

GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC TTC ACC GCG CGG GGA        384
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
               115                 120                 125

CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG GAC GGG GTG AAC TGG        432
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
       130                 135                 140

GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG GTC ATG TGT GTG GAG        480
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160

AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC AAC ATC GCC CTG TGG        528
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
               165                 170                 175

ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC TGG ATC CAG GAT AAC        576
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
               180                 185                 190

GGA GGC TGG GTA GGT GCA TCT GGT GAT GTG AGT CTG GGC                    615
Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
               195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:23:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 205 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1               5               10                  15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
                20                  25                  30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
                35                  40                  45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
        50                  55                  60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65                  70                  75                  80
```

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```
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
             85                   90                   95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
            100                 105                 110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
            115                 120                 125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
    130                 135                 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
            165                 170                 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
            180                 185                 190

Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
        195                 200                 205


(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Other nucleic acid;
        (A) DESCRIPTION: Synthetic DNA

   (iv) ANTI-SENSE: YES

   (ix) FEATURE:
        (A) NAME/KEY: Modified_base
        (B) LOCATION: 16..17
        (D) OTHER INFORMATION: Last two internucleoside linkages are
                phosphorothioates

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
                                                                      18
TCTCCCAGCG TGCGCCAT


(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
```

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(ii) MOLECULE TYPE: Other nucleic acid;
          (A) DESCRIPTION: Synthetic DNA

     (iv) ANTI-SENSE: NO

     (ix) FEATURE:
          (A) NAME/KEY: Modified_base
          (B) LOCATION: 16..17
          (D) OTHER INFORMATION: Last two internucleoside linkages are
               phosphorothioates

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGCACTCACG CTCGGCCT   18

(2) INFORMATION FOR SEQ ID NO:26:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: Other nucleic acid;
          (A) DESCRIPTION: Synthetic DNA

     (iv) ANTI-SENSE: YES

     (ix) FEATURE:
          (A) NAME/KEY: Modified_base
          (B) LOCATION: 18..19
          (D) OTHER INFORMATION: Last two internucleoside linkages are
               phosphorothioates

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCGGCGGG CGGGCGGGCA   20

(2) INFORMATION FOR SEQ ID NO:27:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: Other nucleic acid;
          (A) DESCRIPTION: Synthetic DNA

     (iv) ANTI-SENSE: NO

     (ix) FEATURE:
          (A) NAME/KEY: Modified_base
          (B) LOCATION: 18..19
          (D) OTHER INFORMATION: Last two internucleoside linkages are
               phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGCGGAGGC CGGCCGGCGG   20

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other nucleic acid;
        (A) DESCRIPTION: Synthetic DNA

    (iv) ANTI-SENSE: YES

    (ix) FEATURE:
        (A) NAME/KEY: Modified_base
        (B) LOCATION: 18..19
        (D) OTHER INFORMATION: Last two internucleoside linkages are
            phosphorothioates

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCGGCGGCG GCGGCAGCGC   20

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other nucleic acid;
        (A) DESCRIPTION: Synthetic DNA

    (iv) ANTI-SENSE: NO

    (ix) FEATURE:
        (A) NAME/KEY: Modified_base
        (B) LOCATION: 18..19
        (D) OTHER INFORMATION: Last two internucleoside linkages are
            phosphorothioates

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCCGGGAA GGGCGCCCGC   20